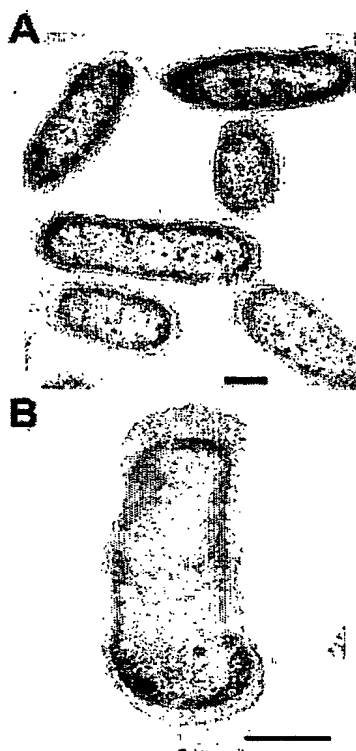


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FIGURES

FIG. 1



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FIG. 2

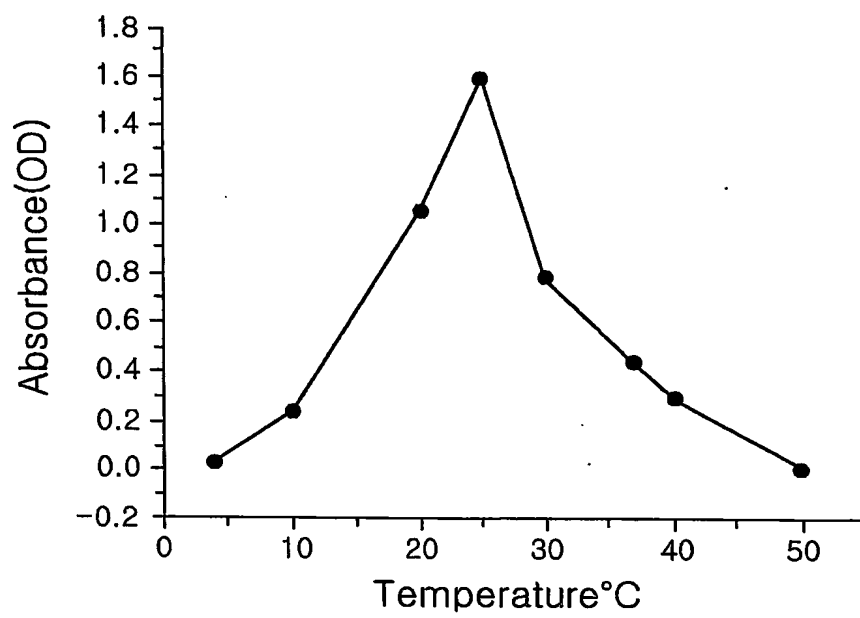
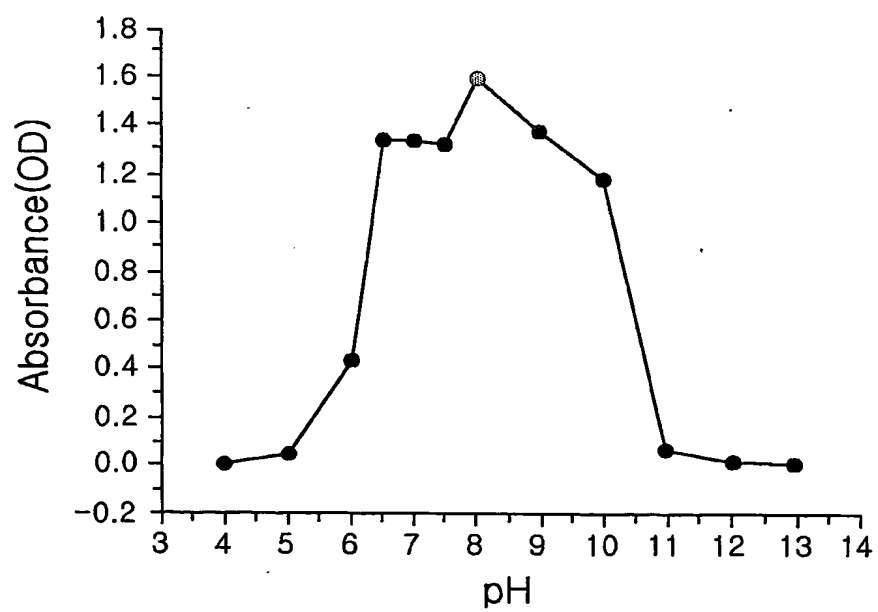


FIG. 3



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FIG. 4

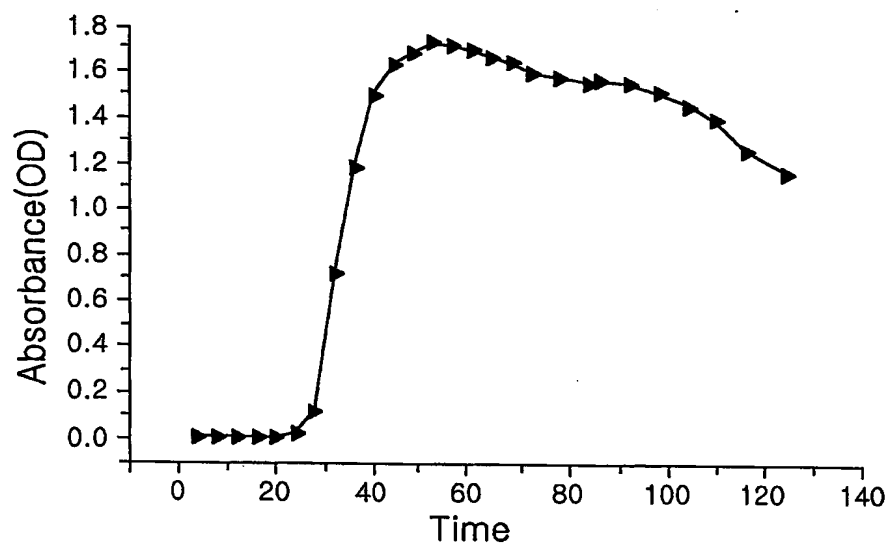
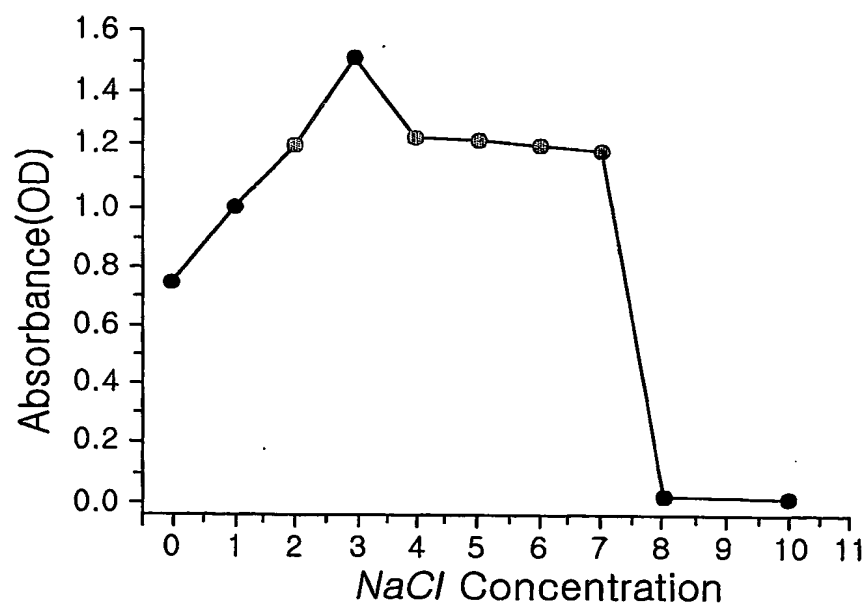
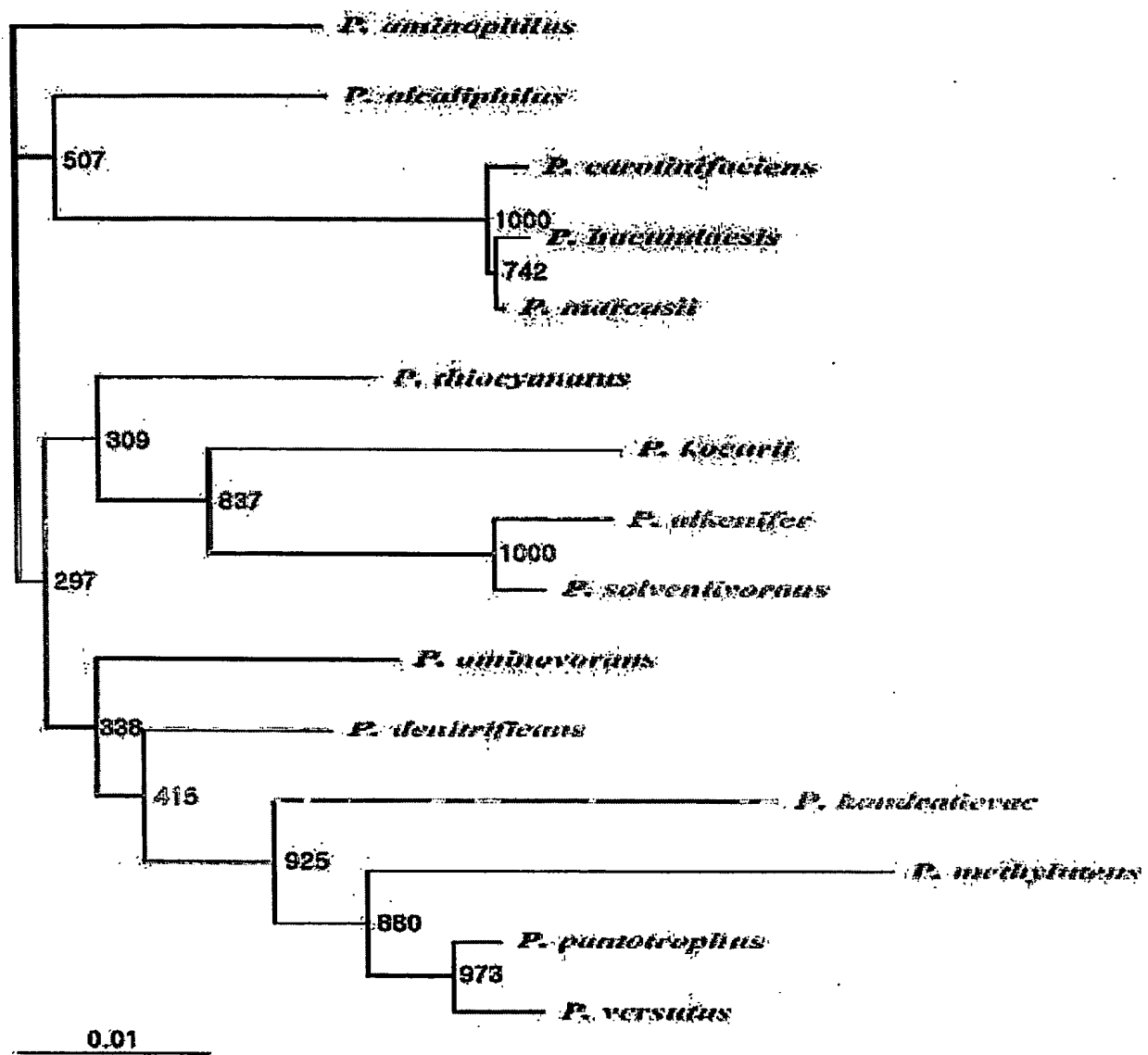


FIG. 5



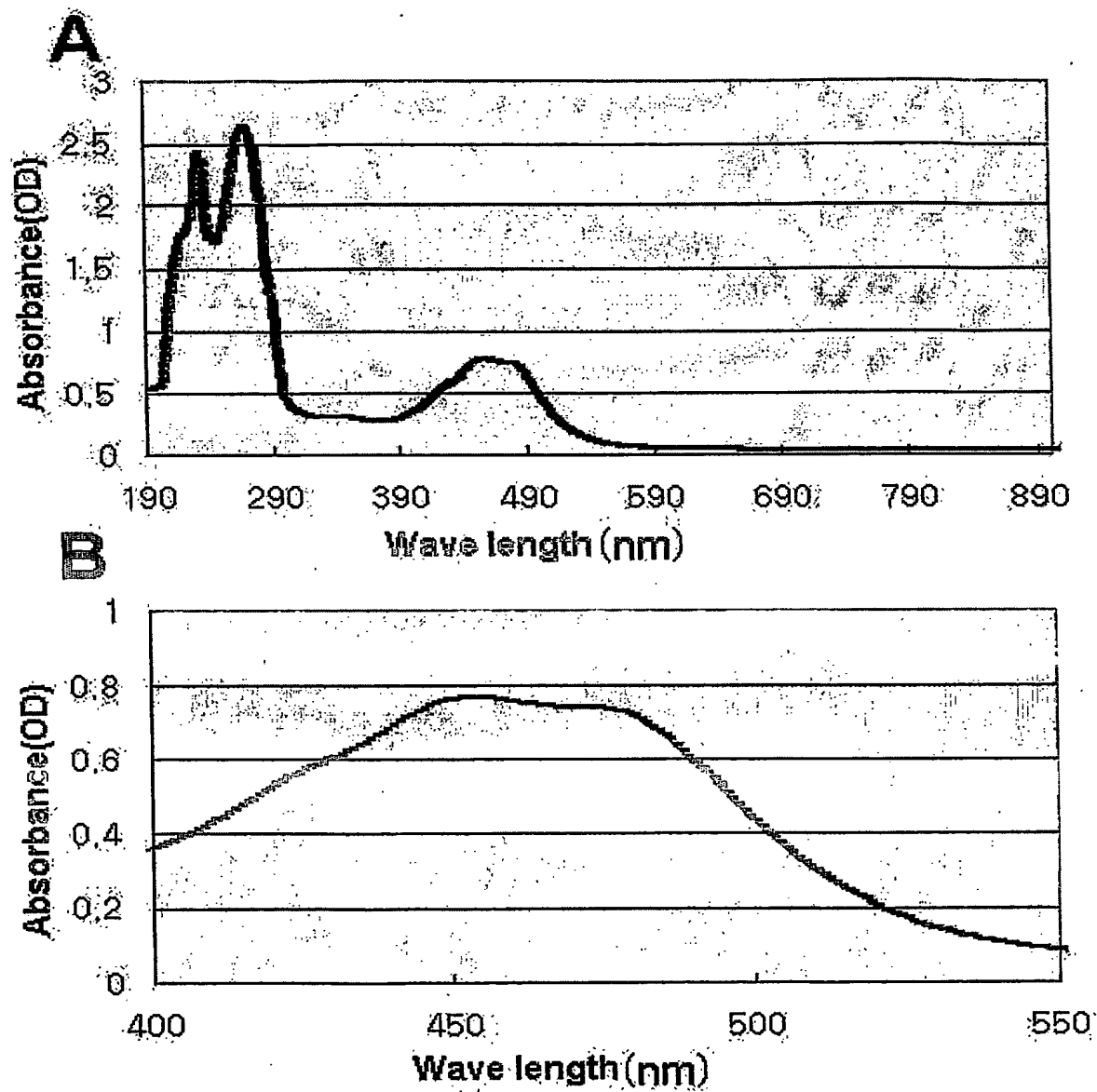
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FIG. 6



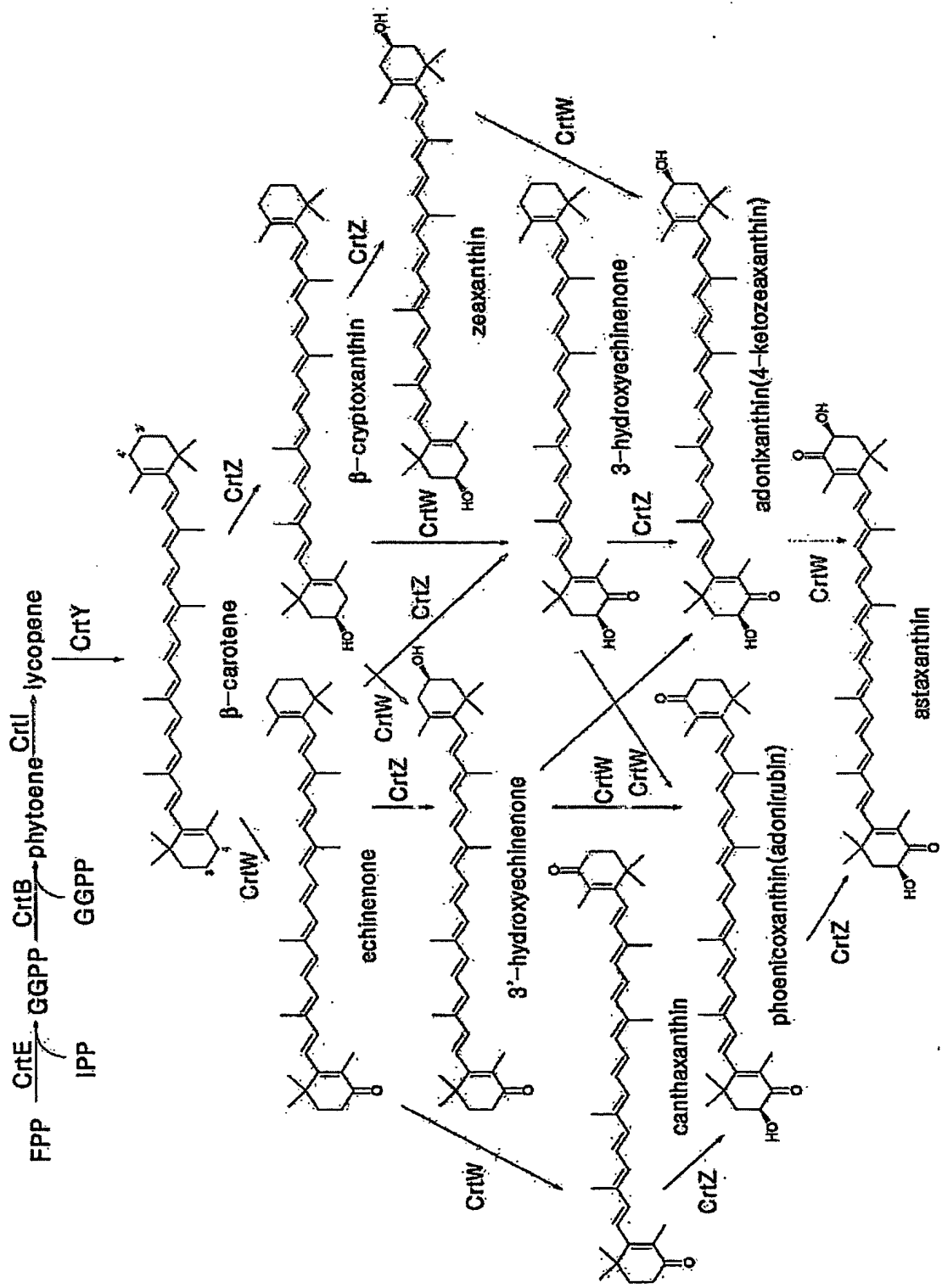
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FIG. 7



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FIG. 8



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FIG. 9

	1		100
<i>P. haerundae</i>	(1)	MSAHALPKADLYATSLIYSGGIIAAVLALHVBALWFLDAAAHPI LAIANELGLT -WLSVGLPFI AHDANHGS VVPGRPBANAAGQLVLE	
<i>Alcaligenes_sp</i>	(1)	MSGREPGTIGDTIYMLGLTAAILLCPLVLAFTLWLDAAAHPLAVLCLAGLT -WLSVGLPFI AHDANHGS VVPGRPBANAAGQLVLE	
<i>Bradyrhizobium_sp</i>	(1)	MHAATAKATEPGASRRDDARQRRVGLTAAVITAAWLVLVGLENFFWPLTSLSLPALPLVVLQVLYVGLFI AHDCHHGS LYPPEQVHRI GQLCLF	
Consensus	(1)	MSA K A T V L LSAALIAAWLVLEV L WFLDAAAHPLAIL LGLT WLSVGLPFI AHDANHGS VVPGRPBANAAGQL LV	
	101		200
<i>P. haerundae</i>	(90)	LYAGFSVRKNI VKHNAHHRHTGTDDDPDQHG---GPVRUYARFIFTFGVREGLLPVI VTYALILGD-RWYVVFVPLPSTILASTQLFVFGTLPBR	
<i>Alcaligenes_sp</i>	(90)	LYAGFSVPKLTAKHNT HHRHAGTDNDPDQHG---GPVRUYGSPVSYFGVREGLLPVI VTYALILGD-RWYVVFVPLPSTILASTQLFVFGTLPBR	
<i>Bradyrhizobium_sp</i>	(101)	LYAGFSFDALNVHHRHHRBPATADLDEDEVPFBQFVHFPASSFLHYFGKQVAITAAVSLVYQLVFAVPLQNLIFPAEPGLLSADQLT FGTTLFBR	
Consensus	(101)	LYAGFSV KLIVKHN HHRH GTDDDPDQHG GPVRUYASFI TYFGVREGLLPVI VTYALILGD RWYVVFVPLPSTILASTQLFVFGTLPBR	
	201		299
<i>P. haerundae</i>	(186)	PGHDAPFDHNAESSRISDPVSLTCTFHFGGVHHEHLHPVFWWLPSTRTKGDTA--	
<i>Alcaligenes_sp</i>	(186)	PGHDAPFDHNAESSRISDPVSLTCTFHFGGVHHEHLHPVFWWLPSTRTKGDTA--	
<i>Bradyrhizobium_sp</i>	(201)	PATQPPADHNAETSEPPAVLSLLTCTFHFG-FHHEHLHPDAPVWLPSTRTKGDTRD	
Consensus	(201)	PGHD APDHNARSS I DPLSLLTCTFHFGGVHHEHLHP VFWWLPSTRTKGD A	

FIG. 10

	1		100
<i>P. haerundae</i>	(1)	HTNFLI VVATVLVHETAYS VHWIINBGPLGUGVHSHHEERDHALEKNDLYGLVFAVIATVLFYGVWVAPVLWVIALGNT VYGLIYFVLHDLGVBRW	
<i>Alcaligenes_sp</i>	(1)	HTNFLI VVATVLVHETAYS VHWIINBGPLGUGVHSHHEERDHALEKNDLYGLVFAVIATVLFYGVWVAPVLWVIALGNT VYGLIYFVLHDLGVBRW	
Consensus	(1)	HTNFLI VVATVLVHETAYS VHWIINBGPLGUGVHSHHEERDHALEKNDLYGLVFAVIATVLFYGVWVAPVLWVIALGNT VYGLIYFVLHDLGVBRW	
	101		163
<i>P. haerundae</i>	(101)	PFRYIPRGGYARLYQABRLHHAVEGRDHCVSFGFIYAPPVOKLQDLKSGVLRBAEQERT	
<i>Alcaligenes_sp</i>	(101)	PFRYIPRGGYARLYQABRLHHAVEGRDHCVSFGFIYAPPVOKLQDLKSGVLRBAEQERT	
Consensus	(101)	PFRYIPRGGY BRLYQABRLHHAVEGRDHCVSFGFIYAPPVOKLQDLK SGVLR S	

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FIG. 11

	1	100
P. haerundaeisis	(1) VIEDVLLAGAGL ANGLIALALBAAREDLVLLDHAAGPSDHTESCHDPLSPHULANLEPLRRANFPDQEVFPFHARBLATGYGSLDGAALADAVAR	
Flavobacterium_sp	(1) MSBLLIAGAGLSGALIALAVDRREDAIRVHLDAESQPSIQHTQCCHUTDLEPEULADLSPIEGEFTDQEVAFPDESERLTTGYGSIAGALIGLLQ-	
Consensus	(1) MSBLLIAGAGLA ALIALALB RPD RILLDD AGPSD HTSCHD DLSF ULARL PIRRA W DQEV FP HARBL TGYGSI DAAAL L	
	101	200
P. haerundaeisis	(101) SGARIEVHS DIALLEDEQAYLS CGTRIEAGAVLDGGAQPSBHLTVGQKFPVGVIEIETDCPQVPPPHINDATVTQQDGYREITLLPFSPTRILIEDTBY	
Flavobacterium_sp	(100) -GVDLRVHTVATLDDTGATITDGSRIEACVIDALQAVETPRLTVQKFPVGVIEIETDAPRQVPPPHINDATVPQMDYRFIVLLPFSPTRILIEDTBY	
Consensus	(101) G DIRVNS IA LDD GATLS GSRIEAA VIDARGA S HLTGQKFPVGVIEIETD PPGV RPHINDATV Q DGYREIVLLPFSPTRILIEDTBY	
	201	300
P. haerundaeisis	(201) SDGYNLDDALAAASHDYARQQGWTGAEEVREERGLIPIALABDAASFVADAEAGFPVPGVGLBAGFEPVYTGZLLYAAQVADVACLSGPPGTDALEGAIB	
Flavobacterium_sp	(189) SNGHLDLGGALAAQLDYAARRQVTHQEMKREBGTPIALAHDAIGFURDHAGATVPVGLGALFPHIVIGTSLPYAAQVADALAAAR--DLTTASARRAVK-	
Consensus	(201) SDGG LDD ALA AS DYA GWTG HRRERBGLIPIALABDA GFW DBA G VPVGL AG FHPVTGYSLPYAAQVAD IAA T A R AIR	
	301	397
P. haerundaeisis	(301) DYALDSAREDEFLRLNRLFRGCAPDRBYTLLQEFVKNPBGHIEGTYAGRLSVADQLRIVIGKPPITPLGTATCLPEEPLEKNA	
Flavobacterium_sp	(297) GWALINADKSRFLELLNRLFRGCPPDRBTRLIQEFVBLPQPLINFTAGMLTLADREIRVYGRPFILSQAIVCLPSEFLQGBA	
Consensus	(301) VADIRA RDRFLRLNRLFRGC PDRBY LLQEFYRLP LIERFYAGRLSLAD LRIVTGKPPITL AIRCLPERPLL E A	

FIG. 12

	1	100
P. haerundaeisis	(1) HNAHSPAARTXITIGAGFGALALAIRLQSAIGATTLYEADDEFGGATVTHDQGVHEDPAGETITDPALEKLELALTOGHARDVTLHPTCFYELHUPG	
Flavobacterium_sp	(1) -----MSSATXIGAGFGALALAIRLQSAIGATTIVBARHFGGATVTHDQGVHEDPAGETVYTPDLSLELWALSQOPHEDVTLLPVSPTFLTQAD	
Consensus	(1) S T VIGAGFGALALAIRLQSAIGATTIVBARHFGGATVTHDQGVHEDPAGETITDPALEKLELWALSQQ N RDVTLPLPVSPTFLTQ	
	101	200
P. haerundaeisis	(101) QEVFDYTHAQLLELQIAQFLADOLEGVIEFRDYAEETVQSGATVLAQVIFLELQETLKAAPALHKLKAYESVNAKVAETIKTPYLDGAFSTYELLVWQH	
Flavobacterium_sp	(94) GRSEFYVHDDDEELIQQVSEFTADVQGVYEFHDAEYVHMGVLEHGTTPRLKLGGLNNAAPALHRLQAYECVHSHVAREFIQDFELGAFSTFELLVQWH	
Consensus	(101) GK FDYVND D L BQIA ENP DLDGYREF DYAREVY EGVLELGT PFLKLGQL AAPALHKL AYESVHA VA FI DPHLRQAFSPHLLVQGN	
	201	300
P. haerundaeisis	(201) PFSTSSIVALIHALLERGGVVPKAGGTQELVAGHVALFERLGGQNNLNAKVAETITDPAATTGVTLADGESLADNATACNVDWHNNYDILLGETALGQSR	
Flavobacterium_sp	(194) PFSTSSIVALIHALLERGGVVEKAGGTINQLVAGHVALFERLGGTLLINAEVTEIDTEEDATGVYLLDGRQLRADTVAENGVHVS YEDLLGHFREGRTK	
Consensus	(201) PFSTSSIVALIHALLERGGVVFAGGTINQLVAGHVALFERLGG LLLNAKV RIDTEG R TGVTL DGR LRAAD VASNGDVH YEDLLGHF REG SK	
	301	400
P. haerundaeisis	(301) ASSLDEKRUSHSIFVLFHGLREAPEDIAHBTILFQPYREIVHETIFRGLAEDEFSLYLBSPTCTDPMAPPGETSYVFAFVFLHGRABIDGAVRGPY	
Flavobacterium_sp	(294) AAILNEQVCHSLFVYHPTSKRPENLABHSVIPGPRTGLVREIENJPRLEDDFSNYLHSTCVTIVSLAEHGSTHYVLAPVPELGRADVDEABAPQV	
Consensus	(301) A L R EWSHSIFVLFHGL P IAHRSIIPGPRTK LVNRIE GPKL DDFSLYLBSPT TDF LAP GHSTHYVLAPVPELGRADIDV EAP Y	
	401	500
P. haerundaeisis	(401) ADRIASLERBLIPNLRAHLITTRIFTPADASHLNABGCAPSVEPIILTQAVFRPHNDKTI RNFTLYGAGTHPGAGIDPQVGS AKAT AQVHLSDLA	
Flavobacterium_sp	(394) AERIPEELERBALPDLRHLTVSEIIPSTADSTELS AHHGSAFVVEPIILTQAVFRPHNDKAI PHEVIVGAGTHPGAGIDPQVGS AKAT AQVHLSDLAV	
Consensus	(401) ADRI LE R IP LR LT SRIFSPADFASL AHHGSAFVVEPIILTQAVFRPHNDK I NFVIVGAGTHPGAGIDPGVGS AKAT AQVHLSDLA	
	501	
P. haerundaeisis	(501) A	

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FIG. 13

	1	100
<i>P. haemdaesis</i>	(1) NSDLVLTSTHAYTQSSQSFATAAKLHPGIRDDTVHLYAECBADDVIDGIALGSRPEAYNDPQARLDGLRVDTLAALQGDSPVTFPAALBAYABRHDF	
<i>Flavobacterium_sp</i>	(1) HTDLTATSEAM AQGSCSFAQAARLMPPGIRDDTVHLYAECBADDVIDGQVMSAPRAGGTPQARLDGLRAVDTIAALHRTGPNSPFPALQGVABRHDF	
Consensus	(1) NSDL TS AI QGSQSF AAKLHPPGIRDDTVHLYAECBADDVIDGQ LGS PSA DPQARL ALR DTLAAL DGPMSPPFAALR VABRHDF	
	101	200
<i>P. haemdaesis</i>	(101) PQAWPHDLIRGFANDVHARDVYTLDDVLEYSTHYAGIVGVHARVHGVYRDPVLDRACDLGLAFCLTNIAARDVIDDARIHCVLPQDGLDQAGARIDGPF	
<i>Flavobacterium_sp</i>	(101) EDLVPMDLIRGFANDVADREYRSLDDVLEYSTHYAGIVGVHARVHGVYRDPVLDRACDLGLAFCLTNIAARDVIDDARIHCVLPADGLARAGATVHSPV	
Consensus	(101) P WPMDLIRGFANDV RDYRSLDDVLEYSTHYAGIVGVHARVHGV DD VLDRACDLGLAFCLTNIAARDVIDDA IGRCLPADWL AGA IDGPF	
	201	300
<i>P. haemdaesis</i>	(201) PSPHLYVLELLDEAEYTYASAEVLADLPPECAVSI AALALITVAIGLRYEKGQAYRQRTSYSKAAKIGLLGVGQVVARSELPGAGVSBQGLRTE	
<i>Flavobacterium_sp</i>	(201) ESDALYSVIIELDAEYTYASAEVLADLPPECAVSI AALALITVAIGLRYEKGQAYRQRTSYSKAAKIGLLGVGQVVARSELPGAGVSBQGLRTE	
Consensus	(201) PS LYSVIIELD AEYTYASAE GL LPPECAVSI AALRIYRIG RIE GP AYEQRISTSKAAKIGLLA GG D A SEL GA ISB GLVTR	
	301	
<i>P. haemdaesis</i>	(301) PHEV	
<i>Flavobacterium_sp</i>	(301) PEA-	
Consensus	(301) P	

FIG. 14

	1	100
<i>P. haemdaesis</i>	(1) URRDVNPINATLLQTLLEETACGTGAVSQPLQAECHGALSSIREFEGHLELLAAEABGGVCDTIYDAACAVETVHNSALICATLLCTTQAGLSCRTA?	
<i>Flavobacterium_sp</i>	(1) YTPKQQPPLDLVHIRLAQISGQGVVSAFLQAAKEDPAALSPKKEFRAVLHLHVABSSQGVCDANVDAACAVETVHNSALIFDDHICHDOARTEEGQPM	
Consensus	(1) N N LL BL IA FG VS PLGAAMS AALS GKRFRAHMLL AEASGGVCD IYDAACAVETVHNSALIFDDLPCHDDA BRG PAT	
	101	200
<i>P. haemdaesis</i>	(101) HVARGESDAVLGQIALITYAHALLAGAGSGITVTAQLVRILSSSLAQQLCAGQDLIRAAKNGAGVEQEDLRTGVLPFAGLEHLAVIEFQAEQDTQ	
<i>Flavobacterium_sp</i>	(101) HVARGESDAVLGQIALITYAHALLAGAGSGITVTAQLVRILSSSLAQQLCAGQDLIRAAKNGAGVEQEDLRTGVLPFAGLEHLAVIEFQAEQDTQ	
Consensus	(101) HVARGE BAVLAGIALITYEAL ILA ARGAS RA LV LSRALGP GLCAGQDLIRAAKNGAGVEQEDLRTGVLPFAGLEHLAVIEFQAEQDTQ	
	201	235
<i>P. haemdaesis</i>	(201) MIDFGKQLGRVFGSYDDLLDVYGVQNALGKITGEDAPAPSPRELLA9SDLNVSRYEASERQLPANLSKRLQAPRIAALELYLPYAAALA--	
<i>Flavobacterium_sp</i>	(201) LNAFGKQLGRVFGSYDDLLDVYGVQNALGKITGEDAPAPSPRELLA9SDLNVSRYEASERQLPANLSKRLQAPRIAALELYLPYAAALA--	
Consensus	(201) LI FGRQLGRVFGSYDDLLDVIGD AA GKDTARD AAPGPK GLLAV L VA HY ASBAQLD LLRSK A IA LL EYLPB R	

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FIG. 15

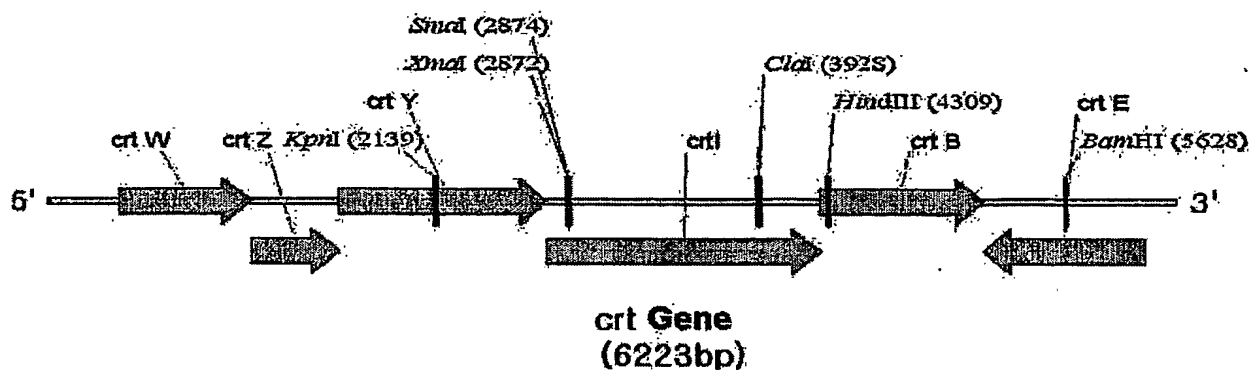
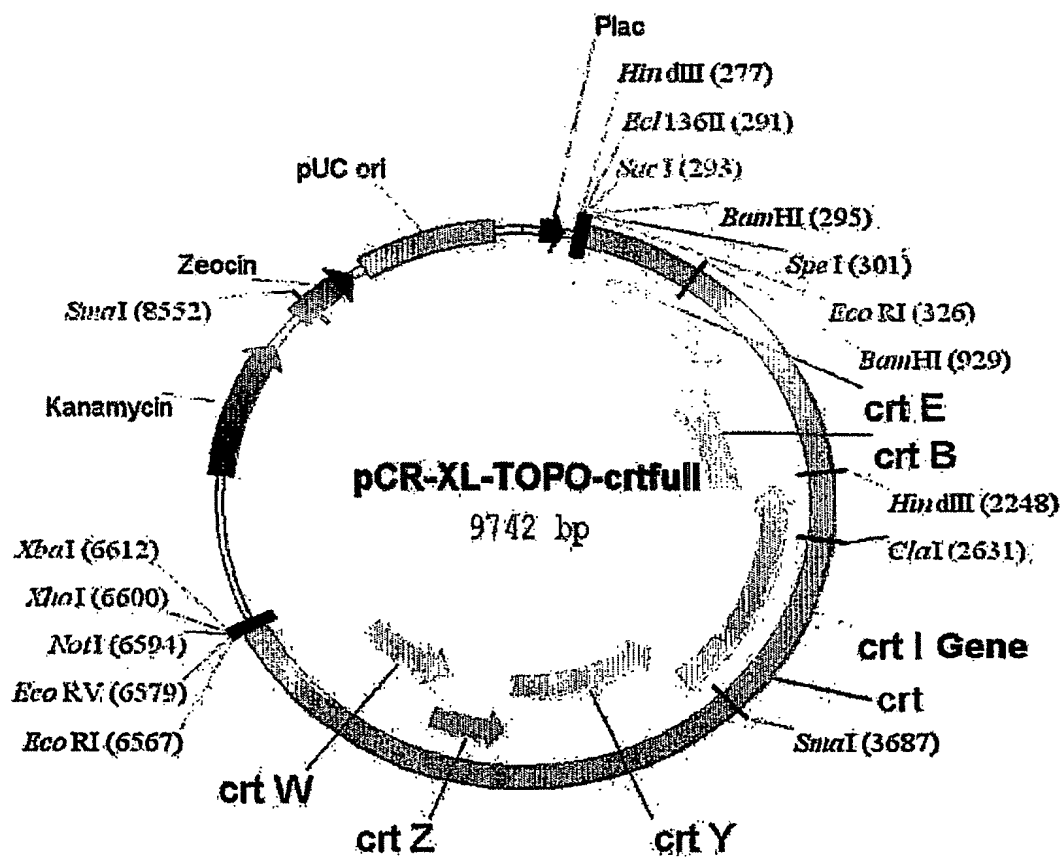


FIG. 16



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FIG. 17

